



- 1 -

# SEQUENCE LISTING

<110> Willson, Tracey  
Nicola , Nicos  
Hilton, Douglas  
Metcalf, Donald  
Zhang , Jian

<120> A novel haemopoietin receptor and genetic sequences encoding same

<130> 23199-215

<140> US 09/688,286

<141> 2000-10-31

<150> AU PN6135

<151> 1995-10-23

<150> AU PN7276

<151> 1995-12-22

<150> AU PP2208

<151> 1996-09-09

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 1680

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (61)..(1332)

<223>

<400> 1

tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgagge gagggcctgc 60

atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108  
Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp  
1 5 10 15

acc gcc acc gtg ggc caa gtt gcc gcg gcc aca gaa gtt cag cca cct 156  
Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro  
20 25 30

gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata tgg 204  
Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp  
35 40 45

ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa act	300
Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr	
65 70 75 80	
cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag gtg	348
His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val	
85 90 95	
ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg gtg	396
Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val	
100 105 110	
aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg act	444
Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr	
115 120 125	
gaq ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc tgg	492
Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp	
130 135 140	
ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac tat	540
Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr	
145 150 155 160	
tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat aga	588
Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg	
165 170 175	
gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa cct	636
Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro	
180 185 190	
agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat gct ggg	684
Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly	
195 200 205	
aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat gtg aaa	732
Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys	
210 215 220	
cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt gcc tta	780
Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu	
225 230 235 240	
tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc tta act	828
Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr	
245 250 255	
tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat att tta	876
Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu	
260 265 270	
gaq gtt gaa gaq gac aaa tcc caq aat tcc gaa tct gat aga aac atg	924

Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val	
290 295 300	
tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt gat gac	1020
Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp	
305 310 315 320	
aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt aag gag	1068
Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu	
325 330 335	
caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca gtc ttt	1116
Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe	
340 345 350	
gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg ctt aag	1164
Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys	
355 360 365	
atc att ata ttt cct cca att cct gat cct ggc aag att ttt aaa gaa	1212
Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu	
370 375 380	
atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag tat gac	1260
Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp	
385 390 395 400	
atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg ctg ata	1308
Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile	
405 410 415	
gaa aac ctg aag aaa gca gct cct tgaatggggag aagtgatttc tttcttgcc	1362
Glu Asn Leu Lys Lys Ala Ala Pro	
420	
tcaatgtgac cctgtgaaga tttattgcat tctccatttg ttatctgggg gacttgtaa	1422
atagaaactg aaactactct tgaaaaacag gcagctocta agagccacag gtcttgatgt	1482
gacttttgca ttgaaaaccc aaacccaaag gagctccttc caagaaaagc aagagttctt	1542
ctcgttcctt gtccaatcc ctaaaagcag atgttttgcc aaatccccc aaactagaggac	1602
aaagacaagg ggacaatgac catcaattca tctaatacagg aattgtgatg gcttcctaag	1662
gaatctctgc ttgctctg	1680

<210> 2  
 <211> 424  
 <212> PRT  
 <213> Mus musculus

Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro  
20 25 30

Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp  
35 40 45

Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr  
50 55 60

Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr  
65 70 75 80

His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val  
85 90 95

Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val  
100 105 110

Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr  
115 120 125

Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp  
130 135 140

Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr  
145 150 155 160

Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg  
165 170 175

Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro  
180 185 190

Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly  
195 200 205

Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys  
210 215 220

Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr  
245 250 255

Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu  
260 265 270

Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met  
275 280 285

Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val  
290 295 300

Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp  
305 310 315 320

Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu  
325 330 335

Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe  
340 345 350

Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys  
355 360 365

Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu  
370 375 380

Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp  
385 390 395 400

Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile  
405 410 415

Glu Asn Leu Lys Lys Ala Ala Pro  
420

<210> 3

<211> 1383

<212> DNA

000 00000

000 00000

<223>

<400> 3

gagtcctaaca cggaccaagg agttaaacaac gtgcggccgg gttccgaggc gagaggctgc	60
atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc	108
Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys	
1 5 10 15	
gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca	156
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro	
20 25 30	
cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata	204
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile	
35 40 45	
tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg	252
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp	
50 55 60	
tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa	300
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu	
65 70 75 80	
act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa	348
Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln	
85 90 95	
gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg	396
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu	
100 105 110	
gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg	444
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val	
115 120 125	
act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct	492
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser	
130 135 140	
tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac	540
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr	
145 150 155 160	
tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt	588
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe	
165 170 175	
aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag	636
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys	
180 185 190	

gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc cgt Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg 210 215 220	732
gtg aaa cct gat cct cca cat att aaa aac ctc tcc ttc cac aat gat Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp 225 230 235 240	780
gac cta tat gtg caa tgg gag aat cca cag aat ttt att agc aga tgc Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys 245 250 255	828
cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn 260 265 270	876
gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag aga Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg 275 280 285	924
aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp 290 295 300	972
act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 305 310 315 320	1020
gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata ggt Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325 330 335	1068
aag aag cgc aat tcc aca ctc tac ata acc atg tta ctc att gtt cca Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro 340 345 350	1116
gtc atc gtc gca ggt gca atc ata gta ctc ctg ctt tac cta aaa agg Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg 355 360 365	1164
ctc aag att att ata ttc cct cca att cct gat cct ggc aag att ttt Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe 370 375 380	1212
aaa gaa atg ttt gga gac cag aat gat gat act ctg cac tgg aag aag Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys 385 390 395 400	1260
tac gac atc tat gag aag caa acc aag gag gaa acc gac tct gta gtg Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val 405 410 415	1308
ctg ata gaa aac ctg aag aaa gcc tct cag tgatgagat aatttatattt	1358

<210> 4  
<211> 426  
<212> PRT  
<213> human

<400> 4

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys  
1 5 10 15

Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro  
20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile  
35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp  
50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu  
65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln  
85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu  
100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val  
115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser  
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr  
145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe  
165 170 175



Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn  
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg  
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp  
225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys  
245 250 255

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn  
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg  
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp  
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr  
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly  
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro  
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg  
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe  
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys  
385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val

425

<400> 5

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser  
20 25 30

<400> 6

31

1. Introduction

<210> 9  
<211> 5  
<212> PRT  
<213> unknown

<220>  
<223> NR4 motif

<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> X may be any amino acid

<400> 9

Trp Ser Xaa Trp Ser  
1 5

<210> 10  
<211> 27  
<212> PRT  
<213> unknown

<220>  
<223> N-terminal amino acid sequence of mNR4 (major)

<220>  
<221> MISC\_FEATURE  
<222> (24)..(24)  
<223> X may be any amino acid

<400> 10

Asp Tyr Lys Asp Asp Asp Tyr Lys Asp Asp Glu Ser Arg Thr  
1 5 10 15

Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val  
20 25

<210> 11  
<211> 27  
<212> PRT  
<213> unknown

<220>  
<223> N-terminal amino acid sequence of mNR4 (minor)

<223> X may be any amino acid

<400> 11

Ala Ser Ile Ser Ser Ser Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr  
1 5 10 15

Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val  
20 25

<210> 12

<211> 5

<212> PRT

<213> unknown

<220>

<223> peptide motif found in many members of the haemopoietin receptor family

<400> 12

Trp Ser Asp Trp Ser  
1 5